

# QUANTITATION OF THE PREMATURE INFANT BRAIN VOLUME FROM MR IMAGES USING WATERSHED TRANSFORM AND BAYESIAN SEGMENTATION

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## ABSTRACT

*Various automated and precise segmentation methods of MR images exist for adult brain, but the segmentation of premature infant brain has been problematic. In this paper, a novel segmentation method for MR images of premature infant brain is proposed. The method utilizes a combination of the watershed transform and bayesian segmentation techniques. An image of intensity gradients is used as a source for the watershed segmentation method. Watershed basins are then combined according to various criteria to produce a set of approximate segment images that can be used to measure the volume of the premature infant brain. The approximate segmentation is then used as a priori information to help bayesian segmentation according to the intensity distributions of the gray matter, white matter and cerebrospinal fluid segments of the brain. The method is compared to a standard segmentation method developed for the brain. The comparison is done for both adult and premature infant brain images.*

## 1. INTRODUCTION

Magnetic Resonance Imaging (MRI) is a 3D medical tomography method that can be used for localization and identification of anatomic structures from tissues. The method is based on the nuclear magnetic resonance technique, which utilizes magnetic fields of high energy. In MR imaging the patient is placed inside a cylinder shaped MRI scanner, where the high magnetic field affects the axes of magnetic spins of hydrogen atoms in tissue so that the axes have the average position with or against the high magnetic field. The spins are then flipped with an electromagnetic radio frequency pulse sequence. After the sequence, the spins return to the alignment of the high magnetic field. The absorbed radio frequency energy is released back and the energy relaxation rate detected by the scanner is used to construct the so-called T1 weighted MRI image. The phase loss of neighbouring spins gives a second relaxation signal T2. The neighbouring spins affect the loss of the phase in spins that is detected by an MRI scanner and is used for the construction of a T2 weighted MRI image.

Image segmentation is a fundamental step in the MR image analysis. In the analysis of brain images, the image is often segmented into three main regions, namely white mat-

ter (WM), gray matter (GM) and cerebrospinal fluid (CSF). CSF is sometimes defined to contain all the regions that do not belong to either GM or WM. Segmentation of MR images is useful, for example, as a pre-step for a large variety of image processing techniques for brain images, such as normalization and co-registration of images for comparative statistical analysis. In this particular study we are interested in segmenting noisy brain data of premature infants. Premature infant brain is a specially demanding object for MR imaging, since the scanning time of children is usually shorter than with adults for safety reasons, although no evidence exists that MR scanning would be harmful for humans. As a downside, the short imaging time reduces the precision of the MR images, which makes the segmentation more difficult. So far the segmentation of the premature infant brain has not been studied in large extent. In [5], part of premature infant brain was segmented using semi-automatic technique utilizing image intensity gradients.

Bayesian brain segmentation [2] is a method that uses *a priori* information of GM, WM, and CSF to bias segmentation in order to eliminate errors affected by noise in the MR images. In the segmentation, a bayesian algorithm is used to determine the three brain segments. For each segment, an *a priori* map is required. The map is based on multiple segmentation results done by human experts for normal adults. However, currently no *a priori* information exists for the premature infant brain. A reason for this is that there are large spatial differences between children of different ages such that it is rather difficult to combine multiple segmentations performed by experts. In order to deal with noisy images without existing *a priori* information, a combination of watershed transform based segmentations of T1 and T2 weighted images is used to create an approximate segmentation. This segmentation is then used as *a priori* map in the bayesian segmentation method to produce the final segmentation. The main idea is thus to replace *a priori* information with segmentation that is based on both spatial information and intensity values. Watershed segmentation has been used earlier in several brain segmentation studies, see for example [11, 6, 8]. In addition to the bayesian and watershed segmentation, brains have been segmented using self organizing maps utilizing T1 weighted, T2 weighted and proton density-weighted scans of same patient [9, 10, 1].

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This article has been organized as follows. The bayesian brain segmentation method is shortly described in section 2. The proposed segmentation method for the premature infant brain images is presented in section 3. Experiments using the proposed technique are reported in section 4 before conclusions in section 5.

## 2. BAYESIAN SEGMENTATION METHOD FOR ADULT BRAIN

SPM2<sup>1</sup> is currently a widely used software package for segmentation of the images of the adult brain. SPM2 applies a bayesian segmentation method by [2]. Predefined probability maps for the three segments are included in SPM2. Each voxel in the input image is represented by an intensity value which is often in the interval [0..255]. The bayesian segmentation method in SPM2 uses the Gaussian Mixture Model (GMM) to cluster these intensity values in three clusters. There are always three components  $p_i(x|\mu_i, \sigma_i)$  ( $i = 1, 2, 3$ ) in the mixture, one for each brain segment. The parameters of the mixture model are computed by a standard expectation maximization (EM) algorithm. In the E-step of the EM algorithm, the probability maps are used to compute the *a posteriori* probabilities for each voxel in position  $t$  with intensity  $x$  to belong to segment  $i$  (WM, GM, CSF).

$$P(i|x, t) = \frac{p_i(x|\mu_i, \sigma_i) \cdot \pi_i}{\sum_{j=1}^3 [p_j(x|\mu_j, \sigma_j) \cdot \pi_j]} \quad (1)$$

where  $\pi_i$  represents the *a priori* probability for voxel at position  $t$  to belong to cluster  $i$ .  $\mu_i$  and  $\sigma_i$  ( $i = 1, \dots, 3$ ) are parameters of the Gaussians determined by the EM algorithm. The *a priori* probabilities  $\pi_i$  are obtained from the *a priori* maps. The propability values bias the *a posteriori* values  $P(i|x, t)$ . The voxels that have similar propability values in *a priori* map tend to be assigned into the same segment by the EM algorithm. The maps are usually constructed so that neighbouring voxels have similar propability values, which results in dependency of the neighbouring voxels in the resulting segmentation. For the premature infant brain no *apriori* maps currently exist. In the next section, we consider the determination of the maps so that we could use the same algorithm for the brain images of the premature infants, too.

## 3. A PRIORI MAPS FOR PREMATURE INFANTS

Since no *a priori* map was available for premature infant brains, other means to generate this information was used. The full process from an MR image to a WM segment image is shown in Fig. 2. T1 and T2 weighted images are first segmented with the watershed segmentation algorithm by [13] using a second order gradient image to define the borders of the watershed regions.

First, the gradient image is calculated for each voxel by using the Sobel operator. The operation is applied to the T1 and T2 weighted images of the patient in order to find borders between the gray matter and the white matter. The average image of the two gradient images is then used for the watershed segmentation. Optionally, bias correction [3] can be applied to T1 and T2 weighted images as a pre-step in order to improve the efficiency of the GMM clustering.

In order to guarantee that all the segments are homogeneous, the segments with high standard deviation are splitted into two segments until the deviation of each segment is below a user specified constant value. The standard deviation is calculated for regions according to the intensity values of the T1 weighted image. In our experiments we have observed that the segmentation result is not very sensitive to the selection of this threshold value. In addition, there is also a fixed minimum size for all the segments. A segment is divided into two subsegments as follows. First, the two points with the largest Euclidean distance in the segment are determined. The two new subsegments are determined using these two extreme points: in the next step, the distance between each voxel of the segment and the two points is computed and each voxel is assigned to the subsegment represented by the nearest extreme point. Because a segment must be connected, this procedure may also result in more than two segments if the shape of the original segment is non-convex, see Fig. 1.

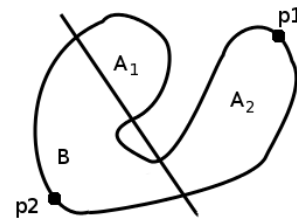


Figure 1: Division of a watershed segment into two subsegments. The subsegment nearest to point  $p1$  is divided into segments  $A_1$  and  $A_2$ .

After region splitting the clustering of the median intensity values of the regions is carried out. The medians are clustered using GMM into three segments: WM, GM, and CSF. The centroids of the three clusters are initialized by using the k-means clustering algorithm. The median values of the clusters are considered to be normally distributed in each cluster. The k-means algorithm is first used as a pre-step to define an initial approximate clustering. Next, the resulting approximate brain regions are averaged with Gaussian kernel in order to create smooth probability maps which are then used as *a priori* information with the T1 weighted image in bayesian segmentation method. The watershed segments of T1 and T2 weighted images are clustered separately and combined together into an approximate segmentation by summing the corresponding probability values of the clustering results for the T1 and T2 weighted images. The T2 weighted results are weighted by correlation values between the corresponding segments in order to enhance segments where the two clustering results agree. We have observed that if CSF is smoothed like the other two segments, parts of the GM are included in the CSF. Therefore we smooth the CSF segment less than GM and WM segments.

## 4. EXPERIMENTS

In order to validate the segmentation results, the proposed method was tested against the segmentation tool of the SPM2 software package. In addition, MR image sets of ten premature infants were segmented and compared to expert measurements.

<sup>1</sup>available at [www.fil.ion.ucl.ac.uk/spm/spm2.html](http://www.fil.ion.ucl.ac.uk/spm/spm2.html)

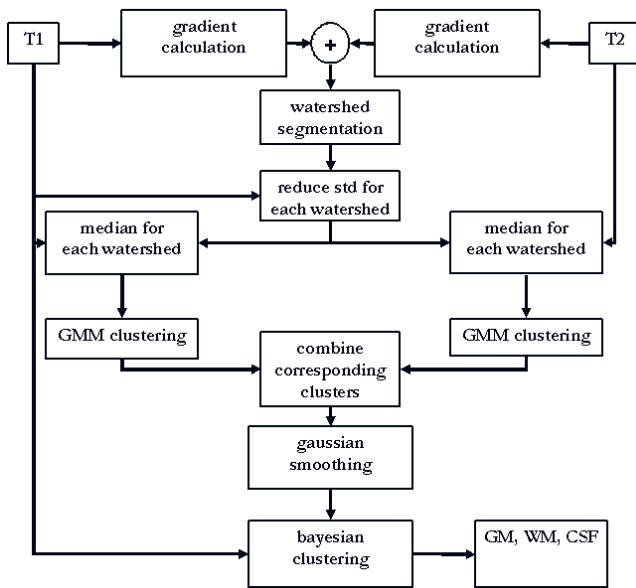


Figure 2: Procedure for watershed based MR segmentation using T1 and T2 weighted MR images of the same patient.

#### 4.1 Comparison to well-known segmentation technique for adult brain

A data set consisting of images of 8 normal adults, scanned with Philips Intera 1.5T MRI scanner, were segmented with our program (referred as W-B) and SPM2, see for example Fig.3. An accustomed brain extraction algorithm [12] was used as a pre-step for our method along with bias correction [3] with SPM2 software package when required. The image matrix sizes were between 256x256x55 and 256x256x89 voxels in the image sets. Voxel sizes were correspondingly between 1mm x 1mm x 1mm and 1mm x 1mm x 2.5mm in each MR image. In segmentation, different parameters were used for weighting the *a priori* maps and the map smoothing kernel size when producing GM, WM and CSF segments.

The non-brain segment was obtained by the brain extraction pre-step. A comparison was carried out with 8 segmented adult brain MR images and confusion matrices against the corresponding SPM2 segmentation were calculated for each patient. The combined confusion matrix is shown in Table 1 where the values represent proportions of the brain gray matter (GM), white matter (WM), cerebrospinal fluid (CSF) and nonbrain segments that were assigned to corresponding segments with SPM2 method.

Agreement of our method with the SPM2 in the GM-WM region was found to be excellent. Differences in the non-brain area were mainly due to the preprocessing step of brain extraction and will be assessed in the future work. Segments of one patient (see Fig. 3) were also compared slice by slice to the corresponding results with the SPM2. Agreement between the methods was good in the WM and CSF segments. The largest deviations between the methods for the GM segment were in the bottom slices, see Fig. 4. Here positive values denote additional voxels with the proposed method and negative values missing voxels, correspondingly.

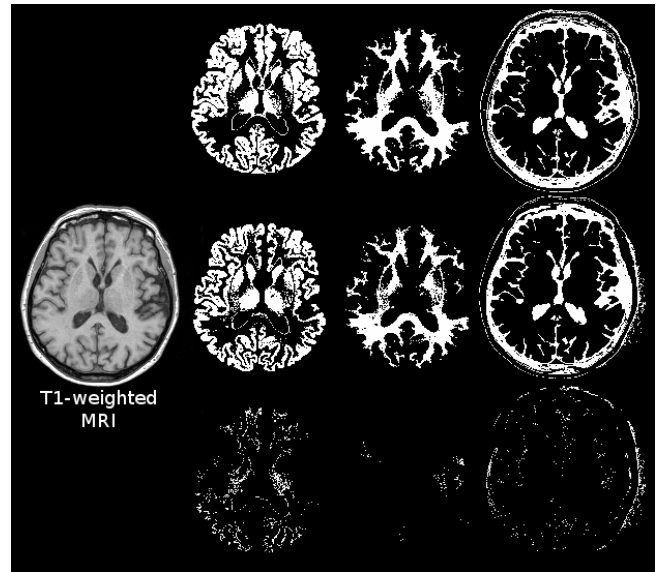


Figure 3: An example of segmentation of an MR image of an adult (on the left). In the first row: T1 weighted MR images divided into GM, WM and CSF segments with SPM2 software. In the second row: corresponding segmentation with the proposed method. In the third row: difference between the segmentations. Slice numbering is from bottom to upwards.

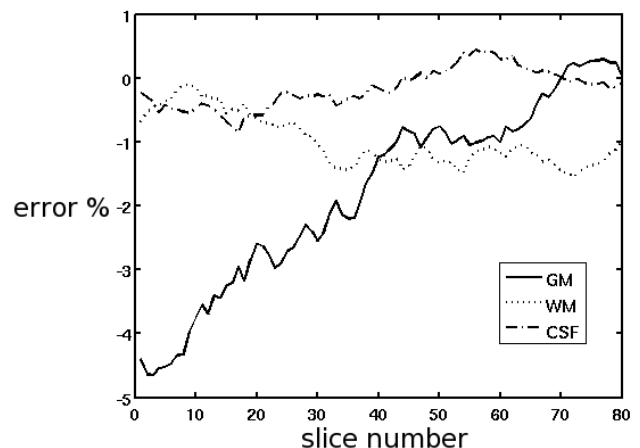


Figure 4: Difference between the proposed method and SPM2 segmentations in 80 slices of an image of an adult brain. The proportions in the figure are relative to the number of voxels in the corresponding slice.

Table 1: The results of the proposed method compared to segmentation using SPM2 software. Agreement of segmentations is shown on diagonal. All the numbers are averages over the 8 images.

		SPM2			
		GM	WM	CSF	non-brain
proposed method	GM	96.5	22.0	0.6	1.4
	WM	0.7	75.1	0.0	1.4
	CSF	2.8	1.3	98.7	44.5
	non-brain	0.0	1.6	0.6	52.8

#### 4.2 Comparison against measurements by an expert

In addition, ten MR images of premature infants were segmented. The full segmentation process took approximately 10 minutes for each image using laptop PC with 1.8 GHz processor. The premature infant image matrix sizes were between 256x256x20 and 256x256x22 voxels and voxel sizes were 0.78mm x 0.78mm x 4.4mm.

The resulting CSF and whole brain volumes were measured and compared against reference segmentation method (SPM2) and the expert measurement, see Fig. 5. At this point, no accurate manual segmentation results by an expert exist. However, ten measurements by an expert were available and used in the comparison of the results (one of original 11 images was discarded from test because of large abnormality). In Fig. 5, two of the brain volume measurements with the proposed method agreed with the results from an expert. However, both of the evaluated methods failed with one image. For the proposed method this is probably due to tendency of the algorithm to bias CSF over GM segment. The volumes of the CSF segment were in alignment with expert measurements. Generally, agreements with the expert measurements were measured with proportions to each expert volume measurement, see Table 2. In the GM-WM region both evaluated methods were generally close to expert measurement. The mean proportion value with SPM2 method in CSF region shows overestimation in that region. There was large deviation in proportional values, especially in CSF region with SPM2 method. Solutions to decrease deviations from expert measurements are left to future work.

Table 2: Agreements of segmented volumes against expert measurements with premature infant MR images. The values represent the mean values of volume proportions to corresponding expert measurement in the GM-WM and CSF regions.

	GM-WM	CSF
SPM2	96.6±6.9	124.8±52.4
proposed method	97.8±13.4	94.7±28.4

## 5. DISCUSSION & CONCLUSION

A novel brain segmentation algorithm was proposed. The algorithm utilizes GMM clustering of watershed segments for creation of *a priori* maps that are not otherwise avail-

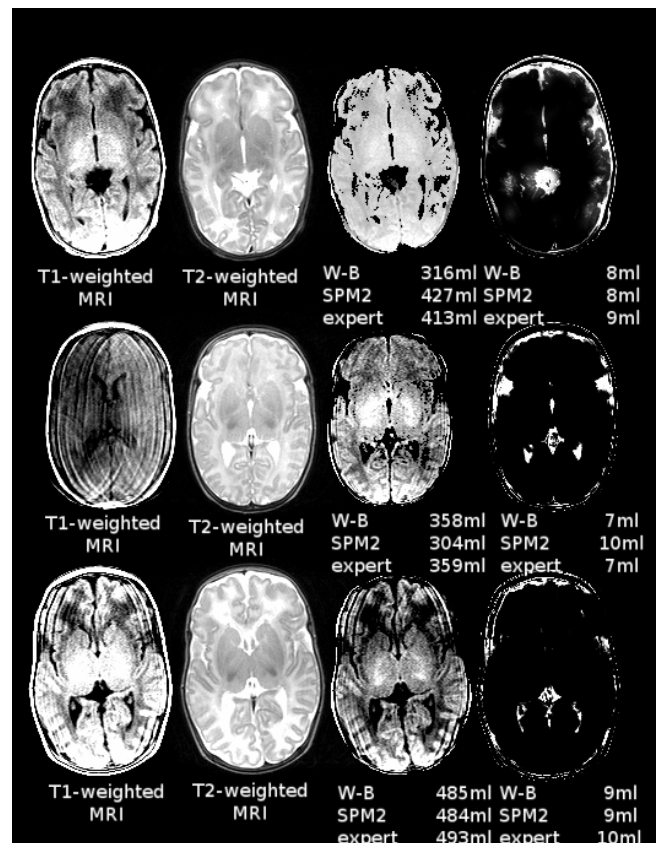


Figure 5: CSF segmentation of the three premature infant MR images. Image slices from left to right: T1 weighted MR image, T2 weighted image, brain segment (GM+WM) and CSF segment. The shown segments are results of watershed-bayesian segmentation method. Volumes of the segments are shown below the corresponding segment images. W-B: watershed-bayesian segmentation method; SPM2: Method included in SPM2 software package; expert: manual volume measurements by an expert.

able for the bayesian segmentation. The principle is to use spatial border definitions acquired with watershed segmentation and clustering of these watershed segments when applying accustomed bayesian segmentation. The method was evaluated against SPM2 software segmentation with 8 adult subjects and brain volume measurements of ten premature infants against expert opinion.

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